

Application No.: 09/787,072  
Amendment and Response dated July 13, 2004  
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**Amendments to the Claims:**

This listing of claims will replace all prior versions and listings of claims in the subject application, and please amend the claims as follows:

1. (currently amended) A method of identifying a nucleic acid sequence involved in ribosomal frameshifting comprising:

1) searching a database of gene sequences to identify sequences which contain the sequence XXX YYY Z, wherein

XXX represents GGG, AAA, TTT or CCC,

YYY represents AAA or TTT,

Z represents A, T, or C

and wherein XXXYYYZ is not AAAAAAA (SEQ ID NO:3) or TTTTTTT (SEQ ID NO:4);

2) further searching among those sequences identified in step 1 for a sequence encoding a pseudoknot structure which is within eight nucleotides of the sequence identified in step 1.

2. (currently amended) The method of claim 1, wherein XXXYYYZ represents a sequence selected from the group consisting of GGG AAA A (SEQ ID NO: 5), GGG AAA T (SEQ ID NO:6), GGG AAA C (SEQ ID NO:7), AAA AAA T (SEQ ID NO:8), AAA AAA C (SEQ ID NO:9), TTT AAA A (SEQ ID NO:10), TTT AAA T (SEQ ID NO:11), TTT AAA C (SEQ ID NO:12), CCC AAA A (SEQ ID NO:13), CCC AAA T (SEQ ID NO:14), CCC AAA C (SEQ ID NO:15), GGG TTT A (SEQ ID NO:16), GGG TTT T (SEQ ID NO:17), GGG TTT C (SEQ ID NO:18), AAA TTT A (SEQ ID NO:19), AAA TTT T (SEQ ID NO:20), AAA TTT C (SEQ ID NO:21), TTT TTT A (SEQ ID NO:22), TTT TTT C (SEQ ID NO:23), CCC TTT A (SEQ ID NO:24), CCC TTT T (SEQ ID NO:25) and CCC TTT C (SEQ ID NO:26).

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3. (original) A method of identifying a nucleic acid sequence involved in ribosomal frameshifting comprising the steps of:

selecting a gene sequence having a sequence of nucleotides from the group of GGG, AAA, TTT and CCC;

selecting said gene sequence having an adjacent sequence of nucleotides from the group of AAA and TTT;

selecting said gene sequence having a nucleotide from the group of A, T and C, said nucleotide adjacent to said adjacent sequence of nucleotides;

excluding said gene sequence wherein said sequence of nucleotides is AAA, said adjacent sequence of nucleotides is AAA and said nucleotide is A;

excluding said gene sequence wherein said sequence of nucleotides is TTT, said adjacent sequence of nucleotides is TTT and said nucleotide is T;

searching for an encoded pseudoknot structure which starts within eight nucleotides of said selected gene sequence.

4. (currently amended) The method of claim 3 wherein XXXYYY represents a sequence selected from the group consisting of GGG AAA A (SEQ ID NO: 5), GGG AAA T (SEQ ID NO:6), GGG AAA C (SEQ ID NO:7), AAA AAA T (SEQ ID NO:8), AAA AAA C (SEQ ID NO:9), TTT AAA A (SEQ ID NO:10), TTT AAA T (SEQ ID NO:11), TTT AAA C (SEQ ID NO:12), CCC AAA A (SEQ ID NO:13), CCC AAA T (SEQ ID NO:14), CCC AAA C (SEQ ID NO:15), GGG TTT A (SEQ ID NO:16), GGG TTT T (SEQ ID NO:17), GGG TTT C (SEQ ID NO:18), AAA TTT A (SEQ ID NO:19), AAA TTT T (SEQ ID NO:20), AAA TTT C (SEQ ID NO:21), TTT TTT A (SEQ ID NO:22), TTT TTT C (SEQ ID NO:23), CCC TTT A (SEQ ID NO:24), CCC TTT T (SEQ ID NO:25) and CCC TTT C (SEQ ID NO:26).

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5. (original) A system for identifying a nucleic acid sequence involved in ribosomal frameshifting, the system comprising:

access means for accessing a database of gene sequences;  
selection means for selecting a particular gene sequence from said database of gene sequences, said particular gene sequence having a sequence of nucleotides from the group of GGG, AAA, TTT and CCC, an adjacent sequence of nucleotides from the group of AAA and TTT, a nucleotide from the group of A, T and C, said nucleotide adjacent to said adjacent sequence of nucleotides, wherein said particular gene sequence is excluded from selection when said sequence of nucleotides is AAA, said adjacent sequence of nucleotides is AAA and said nucleotide is A and said particular gene sequence is excluded from selection when said sequence of nucleotides is TTT, said adjacent sequence of nucleotides is TTT and said nucleotide is T;

pseudoknot search means for locating an encoded pseudoknot structure which starts within eight nucleotides of said selected gene sequence.

6. (currently amended) The system as recited in claim 5 wherein XXXYYYYZ represents a sequence selected from the group consisting of GGG AAA A (SEQ ID NO: 5), GGG AAA T (SEQ ID NO:6), GGG AAA C (SEQ ID NO:7), AAA AAA T (SEQ ID NO:8), AAA AAA C (SEQ ID NO:9), TTT AAA A (SEQ ID NO:10), TTT AAA T (SEQ ID NO:11), TTT AAA C (SEQ ID NO:12), CCC AAA A (SEQ ID NO:13), CCC AAA T (SEQ ID NO:14), CCC AAA C (SEQ ID NO:15), GGG TTT A (SEQ ID NO:16), GGG TTT T (SEQ ID NO:17), GGG TTT C (SEQ ID NO:18), AAA TTT A (SEQ ID NO:19), AAA TTT T (SEQ ID NO:20), AAA TTT C (SEQ ID NO:21), TTT TTT A (SEQ ID NO:22), TTT TTT C (SEQ ID NO:23), CCC TTT A (SEQ ID NO:24), CCC TTT T (SEQ ID NO:25) and CCC TTT C (SEQ ID NO:26).

7. (original) A method of regulating expression of a mammalian gene comprising modulating the frequency of ribosomal frameshifting during translation of messenger RNA.

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8. (original) The method according to claim 7, wherein the frequency of frameshifting is increased.

9. (original) The method according to claim 7, wherein the frequency of frameshifting is decreased.

10. (original) The method according to claim 7, wherein the gene encodes an oncogene.

11. (original) The method according to claim 7, wherein the gene encodes a tumor suppresser gene.

12. (original) The method according to claim 7, wherein the gene encodes a hormone.

13. (original) The method according to claim 7, wherein the gene encodes a human growth hormone.

14. (original) The method according to claim 7, wherein the gene encodes a hormone receptor.

15. (original) The method according to claim 7, wherein the gene encodes a human growth hormone receptor.

16. (original) The method according to claim 6, wherein the gene encodes a catalytic enzyme.

17. (original) A method of treating a disease caused by reducing expression of a gene product which is produced as a result of ribosomal frameshifting, comprising increasing the frequency of ribosomal frameshifting during translation of the gene.

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18. (original) A method of treating a disease caused by increased expression of a gene product which is produced as a result of ribosomal frameshifting, comprising decreasing the frequency of ribosomal frameshifting during translation of the gene.